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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=9; day=23; hr=14; min=11; sec=26; ms=440;]

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Application No: 10554387 Version No: 3.0

Input Set:

Output Set:

Started: 2009-09-22 13:22:09.739
Finished: 2009-09-22 13:22:11.086
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 347 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 14
Actual SeqID Count: 14

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

SEQUENCE LISTING

<110> Protalix Ltd.
 Shaaltiel, Yoseph
 Baum, Gideon
 Hashmueli, Sharon
 Lewkowicz, Ayala
 Bartfeld, Daniel

<120> PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE

<130> 30570

<140> 10554387

<141> 2005-10-25

<150> IL 155588

<151> 2003-04-27

<150> PCT/IL2004/000181

<151> 2004-02-24

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> ER signal peptide

<400> 1

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
 1 5 10 15

Leu Ser Ser Ala Glu Phe
 20

<210> 2

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Vacuolar targeting signal from Tobacco chitinase A

<400> 2

Asp Leu Leu Val Asp Thr Met
 1 5

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 3
 cagaattcgc ccgcccctgc a 21

<210> 4
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 4
 ctcagatctt ggcgatgcca ca 22

<210> 5
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 5
 ctcagaagac cagagggct 19

<210> 6
 <211> 17
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 6
 caaagcggcc atcgtgc 17

<210> 7
 <211> 1491
 <212> DNA
 <213> Homo sapiens

 <400> 7
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acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga	240
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caaaatttgc tacttaaate gtactttctct gaagaaggaa tcggatataa catcatccgg	360
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<210> 8
 <211> 497
 <212> PRT
 <213> Homo sapiens

<400> 8

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys

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Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg	35	40	45
Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly	50	55	60
Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly	65	70	75
Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu	85	90	95
Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu	100	105	110
Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe	115	120	125
Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu	130	135	140
His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu	145	150	155
Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala	165	170	175
Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn	180	185	190
Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr	195	200	205
Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys	210	215	220
Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu	225	230	235
			240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
290 295 300

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
435 440 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
450 455 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
 465 470 475 480

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg
 485 490 495

Gln

<210> 9
 <211> 338
 <212> DNA
 <213> Cauliflower mosaic virus

<400> 9
 ttttcacaaa gggtaatatc gggaaacctc ctcggattcc attgcccagc tatctgtcac 60
 ttcattcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa 120
 ggaaaggcta tcgttcaaga tgctcttacc gacagtggtc ccaaagatgg acccccaccc 180
 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240
 tgtgatattc cactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300
 tcctctatat aaggaagttc atttcatttg gagaggac 338

<210> 10
 <211> 66
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding the ER signal peptide

<400> 10
 atgaagacta atctttttct ctttctcatc ttttcacttc tctatcatt atctcggcc 60
 gaattc 66

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding the vacuolar targeting sequence

<400> 11
 gatcttttag tcgatactat g

<210> 12
 <211> 167
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence of the Agrobacterium tumefaciens terminator

<220>
 <221> misc_feature
 <222> (162)..(162)
 <223> n is a, c, g, or t

<400> 12
 taatttcacg atctgttttg ttgtattccc ttgcaatgca gggcctaggg ctatgaataa 60
 agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg 120
 ttataataa acaaagactt tgtcccaaaa accccccccc cngcaga 167

<210> 13
 <211> 2186
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nucleic acid sequence encoding high mannose human
 glucocerebrosidase (GCD)

<220>
 <221> misc_feature
 <222> (2181)..(2181)
 <223> n is a, c, g, or t

<400> 13
 ttttcacaaa gggtaatatc gggaaacctc ctcggattcc attgcccagc tatctgtcac 60
 ttcacgcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa 120
 ggaaaggcta tcgttcaaga tgccctctacc gacagtgggc ccaaagatgg acccccaccc 180
 acgaggaaca tcgtggaaaa agaagacggt ccaaccacgt cttcaaagca agtggattga 240
 tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300
 tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac 360
 aattaccaac aacaacaaac aacaacaaac attacaatta ctatttacia ttacagtcga 420
 gggatccaag gagatataac aatgaagact aatctttttc tctttctcat cttttcactt 480
 ctctatcat tctctcggc cgaattcgcc cgccctgca tccctaaaag cttcggctac 540

agctcgggtgg tgtgtgtctg caatgccaca tactgtgact cctttgaccc cccgaccttt	600
cctgcccttg gtaccttcag ccgctatgag agtacacgca gtgggcgacg gatggagctg	660
agtatggggc ccatccaggc taatcacacg ggcacaggcc tgctactgac cctgcagcca	720
gaacagaagt tccagaaagt gaagggattt ggagggggcca tgacagatgc tgctgctctc	780
aacatccttg ccctgtcacc ccctgcccaa aatttgctac ttaaatacgta cttctctgaa	840
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acctacacct atgcagacac ccctgatgat ttccagttgc acaacttcag cctcccagag	960
gaagatacca agctcaagat acccctgatt caccgagccc tgcagttggc ccagcgtccc	1020
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atcaaggatc ctgctgtggg cttcctggag acaatctcac ctggctactc cattcacacc	1980
tacctgtggc atcgccaaga tcttttagtc gatactatgt aatttcatga tctgttttgt	2040
tgtattccct tgcaatgcag ggcttagggc tatgaataaa gttaatgtgt gaatgtgtga	2100
atgtgtgatt gtgacctgaa gggatcacga ctataatcgt ttataataaa caaagacttt	2160
gtcccaaaaa ccccccccc ngcaga	2186

<210> 14
 <211> 526
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> High mannose human glucocerebrosidase (GCD)

 <400> 14

 Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
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 Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
 20 25 30

 Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
 35 40 45

 Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
 50 55 60

 Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
 65 70 75 80

 Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
 85 90 95

 Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
 100 105 110

 Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
 115 120 125

 Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
 130 135 140

 Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
 145 150 155 160

 Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
 165 170 175

 Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
 180 185 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys		
195	200	205
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly		
210	215	220
Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp		
225	230	235 240
Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn		
245	250	255
Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly		
260	265	270
Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro		
275	280	285
Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp		
290	295	300
Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp		
305	310	315 320
Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu		
325	330	335
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu		
340	345	350
Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys		
355	360	365
Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln		
370	375	380
Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp		
385	390	395 400
Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val		
405	410	415

Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
420 425 430

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
435 440 445

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
450 455 460

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
465 470 475 480

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
485 490 495

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
500 505 510

Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met
515 520 525